



SEQUENCE LISTING

<110> Staunton, Donald E.

<120> MATERIALS AND METHODS TO MODULATE LIGAND BINDING/ENZYMATIC ACTIVITY  
OF ALPHA/BETA PROTEINS CONTAINING AN ALLOSTERIC REGULATORY SITE

<130> 27866/36470A

<140> 09/976,935

<141> 2001-10-12

<150> US 60/239,750

<151> 2000-10-12

<160> 36

<170> PatentIn version 3.1

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34

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<213> Amino acid insertion

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Pro Lys Gly Arg His Arg Gly Val Thr Val Val Arg Ser His His Gly  
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Val Leu Ile Cys Ile Gln Val Leu Val Arg Arg  
20 25

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gaggggaagc ttagtggggcc 20

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<213> primer Eo-24

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ctgcacatgg tctgggcccgc ctctctc	27
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<213> primer Ecad5'Kozak	
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gcgttaaagc ttcacagctc atcaccatgg gcccttggag ccgca	45
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aggcgctcga gaatccccag aatggcagga att	33
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 <213> primer MAdCAM-1 5'#1

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 atggatttcg gactggccct cctgct 26

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 ctccaagcca ggcagcctca tcgt 24

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 gcgttaaagc ttcacagctc atcaccatgg atttcggact ggcctcct 49

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 <213> Primer Mad 3' #6 Sal

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 gctagtcgac ggggatggcc tggcggtggc tgagctccaa gcaggcagcc tcatcgt 57

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 <213> Primer Alpha1.5

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<213> A1.I.Bam

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<213> Primer specific for 5'ECHPPK

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gtagatgaca gtggcgtata tt

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<213> Primer specific for 3'ECHPPK

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<213> amino acid sequence of ???

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Met Thr Val Ala Tyr Ile Ala Ile Gly Ser Asn Leu Ala Ser Pro Leu  
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Glu Gln Val Asn Ala Ala Leu Lys Ala Leu Gly Asp Ile Pro Glu Ser  
20 25 30

His Ile Leu Thr Val Ser Ser Phe Tyr Arg Thr Pro Pro Leu Gly Pro  
35 40 45

Gln Asp Gln Pro Asp Tyr Leu Asn Ala Ala Val Ala Leu Glu Thr Ser  
50 55 60

Leu Ala Pro Glu Glu Leu Leu Asn His Thr Gln Arg Ile Glu Leu Gln  
65 70 75 80

Gln Gly Arg Val Arg Lys Ala Glu Arg Trp Gly Pro Arg Thr Leu Asp  
85 90 95

Leu Asp Ile Met Leu Phe Gly Asn Glu Val Ile Asn Thr Glu Arg Leu  
100 105 110

Thr Val Pro His Tyr Asp Met Lys Asn Arg Gly Phe Met Leu Trp Pro  
115 120 125

Leu Phe Glu Ile Ala Pro Glu Leu Val Phe Pro Asp Gly Glu Met Leu  
130 135 140

Arg Gln Ile Leu His Thr Arg Ala Phe Asp Lys Leu Asn Lys Trp  
145 150 155

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<212> PRT

<213> ????



<400> 31

Met Gly His His His His His His Gly Gly  
1 5 10

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<212> DNA

<213> 5'EchisHPPK

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cgccatgggc caccaccacc accaccacgg cggcatgaca gtggcgtata tt 52

<210> 33

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<212> DNA

<213> 3'EcXhoHPPK

<400> 33

cggctcgagt taccatttgt ttaatttgt 29

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<211> 169

<212> PRT

<213> amino acid sequence of His(6)-HPPK gene

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Met Gly His His His His His His Gly Gly Met Thr Val Ala Tyr Ile  
1 5 10 15

Ala Ile Gly Ser Asn Leu Ala Ser Pro Leu Glu Gln Val Asn Ala Ala  
20 25 30

Leu Lys Ala Leu Gly Asp Ile Pro Glu Ser His Ile Leu Thr Val Ser  
35 40 45

Ser Phe Tyr Arg Thr Pro Pro Leu Gly Pro Gln Asp Gln Pro Asp Tyr  
50 55 60

Leu Asn Ala Ala Val Ala Leu Glu Thr Ser Leu Ala Pro Glu Glu Leu  
65 70 75 80

Leu Asn His Thr Gln Arg Ile Glu Leu Gln Gln Gly Arg Val Arg Lys  
85 90 95

Ala Glu Arg Trp Gly Pro Arg Thr Leu Asp Leu Asp Ile Met Leu Phe  
100 105 110

Gly Asn Glu Val Ile Asn Thr Glu Arg Leu Thr Val Pro His Tyr Asp  
115 120 125

Met Lys Asn Arg Gly Phe Met Leu Trp Pro Leu Phe Glu Ile Ala Pro  
130 135 140

Glu Leu Val Phe Pro Asp Gly Glu Met Leu Arg Gln Ile Leu His Thr  
145 150 155 160

Arg Ala Phe Asp Lys Leu Asn Lys Trp  
165

<210> 35

<211> 180

<212> PRT

<213> amino acid sequence of LFA-1 I domain

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Gly Asn Val Asp Leu Val Phe Leu Phe Asp Gly Ser Met Ser Leu Gln  
1 5 10 15

Pro Asp Glu Phe Gln Lys Ile Leu Asp Phe Met Lys Asp Val Met Lys  
20 25 30

Lys Leu Ser Asn Thr Ser Tyr Gln Phe Ala Ala Val Gln Phe Ser Thr  
35 40 45

Ser Tyr Lys Thr Glu Phe Asp Phe Ser Asp Tyr Val Lys Trp Lys Asp  
50 55 60

Pro Asp Ala Leu Leu Lys His Val Lys His Met Leu Leu Leu Thr Asn  
65 70 75 80

Thr Phe Gly Ala Ile Asn Tyr Val Ala Thr Glu Val Phe Arg Glu Glu  
85 90 95

Leu Gly Ala Arg Pro Asp Ala Thr Lys Val Leu Ile Ile Ile Thr Asp  
100 105 110

Gly Glu Ala Thr Asp Ser Gly Asn Ile Asp Ala Ala Lys Asp Ile Ile  
115 120 125

Arg Tyr Ile Ile Gly Ile Gly Lys His Phe Gln Thr Lys Glu Ser Gln  
130 135 140

Glu Thr Leu His Lys Phe Ala Ser Lys Pro Ala Ser Glu Phe Val Lys  
145 150 155 160

Ile Leu Asp Thr Phe Glu Lys Leu Lys Asp Leu Phe Thr Glu Leu Gln  
165 170 175

Lys Lys Ile Tyr  
180

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<213> amino acid sequence of LFA-1

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Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly  
1 5 10 15

Phe Phe Phe Phe Ala Pro Ala Ser Ser Tyr Asn Leu Asp Val Arg Gly  
20 25 30

Ala Arg Ser Phe Ser Pro Pro Arg Ala Gly Arg His Phe Gly Tyr Arg  
35 40 45

Val Leu Gln Val Gly Asn Gly Val Ile Val Gly Ala Pro Gly Glu Gly  
50 55 60

Asn Ser Thr Gly Ser Leu Tyr Gln Cys Gln Ser Gly Thr Gly His Cys  
65 70 75 80

Leu Pro Val Thr Leu Arg Gly Ser Asn Tyr Thr Ser Lys Tyr Leu Gly  
85 90 95

Met Thr Leu Ala Thr Asp Pro Thr Asp Gly Ser Ile Leu Ala Cys Asp  
100 105 110

Pro Gly Leu Ser Arg Thr Cys Asp Gln Asn Thr Tyr Leu Ser Gly Leu  
 115 120 125

Cys Tyr Leu Phe Arg Gln Asn Leu Gln Gly Pro Met Leu Gln Gly Arg  
 130 135 140

Pro Gly Phe Gln Glu Cys Ile Lys Gly Asn Val Asp Leu Val Phe Leu  
 145 150 155 160

Phe Asp Gly Ser Met Ser Leu Gln Pro Asp Glu Phe Gln Lys Ile Leu  
 165 170 175

Asp Phe Met Lys Asp Val Met Lys Lys Leu Ser Asn Thr Ser Tyr Gln  
 180 185 190

Phe Ala Ala Val Gln Phe Ser Thr Ser Tyr Lys Thr Glu Phe Asp Phe  
 195 200 205

Ser Asp Tyr Val Lys Trp Lys Asp Pro Asp Ala Leu Leu Lys His Val  
 210 215 220

Lys His Met Leu Leu Leu Thr Asn Thr Phe Gly Ala Ile Asn Tyr Val  
 225 230 235 240

Ala Thr Glu Val Phe Arg Glu Glu Leu Gly Ala Arg Pro Asp Ala Thr  
 245 250 255

Lys Val Leu Ile Ile Ile Thr Asp Gly Glu Ala Thr Asp Ser Gly Asn  
 260 265 270

Ile Asp Ala Ala Lys Asp Ile Ile Arg Tyr Ile Ile Gly Ile Gly Lys  
 275 280 285

His Phe Gln Thr Lys Glu Ser Gln Glu Thr Leu His Lys Phe Ala Ser  
 290 295 300

Lys Pro Ala Ser Glu Phe Val Lys Ile Leu Asp Thr Phe Glu Lys Leu  
 305 310 315 320

Lys Asp Leu Phe Thr Glu Leu Gln Lys Lys Ile Tyr Val Ile Glu Gly  
 325 330 335

Thr Ser Lys Gln Asp Leu Thr Ser Phe Asn Met Glu Leu Ser Ser Ser  
 340 345 350

Gly Ile Ser Ala Asp Leu Ser Arg Gly His Ala Val Val Gly Ala Val  
 355 360 365

Gly Ala Lys Asp Trp Ala Gly Gly Phe Leu Asp Leu Lys Ala Asp Leu  
 370 375 380

Gln Asp Asp Thr Phe Ile Gly Asn Glu Pro Leu Thr Pro Glu Val Arg  
 385 390 395 400

Ala Gly Tyr Leu Gly Tyr Thr Val Thr Trp Leu Pro Ser Arg Gln Lys  
 405 410 415

Thr Ser Leu Leu Ala Ser Gly Ala Pro Arg Tyr Gln His Met Gly Arg  
 420 425 430

Val Leu Leu Phe Gln Glu Pro Gln Gly Gly Gly His Trp Ser Gln Val  
 435 440 445

Gln Thr Ile His Gly Thr Gln Ile Gly Ser Tyr Phe Gly Gly Glu Leu  
 450 455 460

Cys Gly Val Asp Val Asp Gln Asp Gly Glu Thr Glu Leu Leu Leu Ile  
 465 470 475 480

Gly Ala Pro Leu Phe Tyr Gly Glu Gln Arg Gly Gly Arg Val Phe Ile  
 485 490 495

Tyr Gln Arg Arg Gln Leu Gly Phe Glu Glu Val Ser Glu Leu Gln Gly  
 500 505 510

Asp Pro Gly Tyr Pro Leu Gly Arg Phe Gly Glu Ala Ile Thr Ala Leu  
 515 520 525

Thr Asp Ile Asn Gly Asp Gly Leu Val Asp Val Ala Val Gly Ala Pro  
 530 535 540

Leu Glu Glu Gln Gly Ala Val Tyr Ile Phe Asn Gly Arg His Gly Gly  
 545 550 555 560

Leu Ser Pro Gln Pro Ser Gln Arg Ile Glu Gly Thr Gln Val Leu Ser  
 565 570 575

Gly Ile Gln Trp Phe Gly Arg Ser Ile His Gly Val Lys Asp Leu Glu  
 580 585 590

Gly Asp Gly Leu Ala Asp Val Ala Val Gly Ala Glu Ser Gln Met Ile  
 595 600 605

Val Leu Ser Ser Arg Pro Val Val Asp Met Val Thr Leu Met Ser Phe  
 610 615 620

Ser Pro Ala Glu Ile Pro Val His Glu Val Glu Cys Ser Tyr Ser Thr  
625 630 635 640

Ser Asn Lys Met Lys Glu Gly Val Asn Ile Thr Ile Cys Phe Gln Ile  
645 650 655

Lys Ser Leu Tyr Pro Gln Phe Gln Gly Arg Leu Val Ala Asn Leu Thr  
660 665 670

Tyr Thr Leu Gln Leu Asp Gly His Arg Thr Arg Arg Arg Gly Leu Phe  
675 680 685

Pro Gly Gly Arg His Glu Leu Arg Arg Asn Ile Ala Val Thr Thr Ser  
690 695 700

Met Ser Cys Thr Asp Phe Ser Phe His Phe Pro Val Cys Val Gln Asp  
705 710 715 720

Leu Ile Ser Pro Ile Asn Val Ser Leu Asn Phe Ser Leu Trp Glu Glu  
725 730 735

Glu Gly Thr Pro Arg Asp Gln Arg Ala Gln Gly Lys Asp Ile Pro Pro  
740 745 750

Ile Leu Arg Pro Ser Leu His Ser Glu Thr Trp Glu Ile Pro Phe Glu  
755 760 765

Lys Asn Cys Gly Glu Asp Lys Lys Cys Glu Ala Asn Leu Arg Val Ser  
770 775 780

Phe Ser Pro Ala Arg Ser Arg Ala Leu Arg Leu Thr Ala Phe Ala Ser  
785 790 795 800

Leu Ser Val Glu Leu Ser Leu Ser Asn Leu Glu Glu Asp Ala Tyr Trp  
805 810 815

Val Gln Leu Asp Leu His Phe Pro Pro Gly Leu Ser Phe Arg Lys Val  
820 825 830

Glu Met Leu Lys Pro His Ser Gln Ile Pro Val Ser Cys Glu Glu Leu  
835 840 845

Pro Glu Glu Ser Arg Leu Leu Ser Arg Ala Leu Ser Cys Asn Val Ser  
850 855 860

Ser Pro Ile Phe Lys Ala Gly His Ser Val Ala Leu Gln Met Met Phe  
865 870 875 880

Asn Thr Leu Val Asn Ser Ser Trp Gly Asp Ser Val Glu Leu His Ala  
 885 890 895

Asn Val Thr Cys Asn Asn Glu Asp Ser Asp Leu Leu Glu Asp Asn Ser  
 900 905 910

Ala Thr Thr Ile Ile Pro Ile Leu Tyr Pro Ile Asn Ile Leu Ile Gln  
 915 920 925

Asp Gln Glu Asp Ser Thr Leu Tyr Val Ser Phe Thr Pro Lys Gly Pro  
 930 935 940

Lys Ile His Gln Val Lys His Met Tyr Gln Val Arg Ile Gln Pro Ser  
 945 950 955 960

Ile His Asp His Asn Ile Pro Thr Leu Glu Ala Val Val Gly Val Pro  
 965 970 975

Gln Pro Pro Ser Glu Gly Pro Ile Thr His Gln Trp Ser Val Gln Met  
 980 985 990

Glu Pro Pro Val Pro Cys His Tyr Glu Asp Leu Glu Arg Leu Pro Asp  
 995 1000 1005

Ala Ala Glu Pro Cys Leu Pro Gly Ala Leu Phe Arg Cys Pro Val  
 1010 1015 1020

Val Phe Arg Gln Glu Ile Leu Val Gln Val Ile Gly Thr Leu Glu  
 1025 1030 1035

Leu Val Gly Glu Ile Glu Ala Ser Ser Met Phe Ser Leu Cys Ser  
 1040 1045 1050

Ser Leu Ser Ile Ser Phe Asn Ser Ser Lys His Phe His Leu Tyr  
 1055 1060 1065

Gly Ser Asn Ala Ser Leu Ala Gln Val Val Met Lys Val Asp Val  
 1070 1075 1080

Val Tyr Glu Lys Gln Met Leu Tyr Leu Tyr Val Leu Ser Gly Ile  
 1085 1090 1095

Gly Gly Leu Leu Leu Leu Leu Leu Ile Phe Ile Val Leu Tyr Lys  
 1100 1105 1110

Val Gly Phe Phe Lys Arg Asn Leu Lys Glu Lys Met Glu Ala Gly  
 1115 1120 1125

Arg Gly Val Pro Asn Gly Ile Pro Ala Glu Asp Ser Glu Gln Leu  
1130 1135 1140

Ala Ser Gly Gln Glu Ala Gly Asp Pro Gly Cys Leu Lys Pro Leu  
1145 1150 1155

His Glu Lys Asp Ser Glu Ser Gly Gly Gly Lys Asp  
1160 1165 1170